

PERSONS LISTING

(i) GENERAL INFORMATION:

- (ii) APPLICANT: Iris Becker, Israel Vlodavsky and Elena Feinstein
- (iii) TITLE & INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPATOPROTECTIVE ACTIVITY AND EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
- (iiii) NUMBER OF PAGES: 47
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
- (B) STREET: Joel Jefferson Davis Highway, Suite 1007
- (C) CITY: Arlington
- (D) STATE: Virginia
- (E) COUNTRY: United States of America
- (F) ZIP: 22202
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
- (B) COMPUTER: Twinhead* Slimnote-890TX
- (C) OPERATING SYSTEM: MS DOS version 6.2, Windows version 3.11
- (D) SOFTWARE: Word for Windows version 2.0 converted to an ASCII file
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/922,170
- (B) FILING DATE: 2 SEP 1997
- (A) APPLICATION NUMBER: 09/109,386
- (B) FILING DATE: 10 JUL 1998
- (A) APPLICATION NUMBER: PCT/US98/17954
- (B) FILING DATE: 31 AUG 1998
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Friedman, Mark M.
- (B) REGISTRATION NUMBER: 33,883
- (C) REFERENCE/DOCKET NUMBER: 910/14
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 972-3-5625553
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- (C) TELEX:

INFORMATION PROVIDED BY APPLICANT:

- (i) PERSONAL INFORMATION:
- (A) NAME:
- (B) TITLE:
- (C) ORGANIZATION:
- (D) ADDRESS:
- (E) CITY:
- (F) STATE:
- (G) COUNTRY:
- (H) ZIP:
- (ii) PERSONAL INFORMATION OF APPLICANT:
- (A) NAME:
- (B) TITLE:
- (C) ORGANIZATION:
- (D) ADDRESS:
- (E) CITY:
- (F) STATE:
- (G) COUNTRY:
- (H) ZIP:

GTATGATCCATCAATCAATCAATCAAT

(1) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ACTCACTATA GGCCTCAAGC GCG 19

(1) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCATCTTACG CGCTTTTCTT CG 22

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTTTTTTTTT TTTT 15

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTTGATGCA AGAAGCAATC AAC 23

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTATGATCCATCAATCAATCAATCAAT

(1) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5

(A)	LENGTH:	1751
(B)	TYPE:	single - 1000
(C)	STANDARD WEIGHT:	30000
(D)	TOTAL LOSS:	11000

CTAGAGTCTTT	CGACTCTTCT	CTCTGAGGTA	GTGTGGGAG	GATGAGGTA	CTTAGGCTTA	60
AAATGTTGTT	CAATTTAAAG	CTTCTGTTAT	CTTCTGTTAT	ATCTCTGTT	CTTCTGTTAT	120
CTTTGGCTT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	180
CTTTGGCTT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	240
CTTTGGCTT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	300
CTTTGGCTT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	360
CTTTGGCTT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	420
CTTTGGCTT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	480
CTTTGGCTT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	540
CTTTGGCTT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	600
CTTTGGCTT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	660
CTTTGGCTT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	720
CTTTGGCTT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	780
CTTTGGCTT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	840
CTTTGGCTT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	900
CTTTGGCTT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	960
CTTTGGCTT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	1020
CTTTGGCTT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	1080
CTTTGGCTT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	1140
CTTTGGCTT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	1200
CTTTGGCTT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	1260
CTTTGGCTT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	1320
CTTTGGCTT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	1380
CTTTGGCTT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	1440
CTTTGGCTT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	1500
CTTTGGCTT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	1560
CTTTGGCTT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	1620
CTTTGGCTT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	1680
CTTTGGCTT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	CTTCTGTTAT	1740

As a result, the β values are not directly comparable across the different studies. However, the β values are generally in the same order of magnitude, indicating that the effect of the independent variables on the dependent variable is similar across the different studies.

1. *Chlorophyll a* and *Chlorophyll b* were determined by the method of Arar and Collins (1971) using a Shimadzu 1010 UV-Visible Spectrophotometer.

[illegible]

M + Dec Dec Apr Sep May E All Dec E E E Dec M + Dec Dec

+ + +

Leu Leu Gly Pro Leu Gly Trp Leu Ser Pro Gly Ala Ser Trp Ala Pro

65	70	75	80
Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly			
85	90	95	
Thr Lys Thr Asp Phe Leu Ile Phe Asp Ile Lys Lys Gln Ser Thr Phe			
100	105	110	
Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys			
115	120	125	
Tyr Gly Ser Ile Pro Pro Asp Val Glu Gln Lys Leu Arg Leu Glu Trp			
130	135	140	
Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe			
145	150	155	160
Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe			
165	170	175	
Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu			
180	185	190	
Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu			
195	200	205	
Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn			
210	215	220	
Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser			
225	230	235	240
Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys Ser			
245	250	255	
Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg			
260	265	270	
Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Gln			
275	280	285	

Val Ile Asp Ser Val Thr Trp His His Thr Tyr Leu Asn Gly Arg Thr			
290	295	300	
Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile			
305	310	315	320
Ser Ser Val Glu Lys Val Phe Gln Val Val Gln Ser Thr Arg Ile Gly			
325	330	335	

Val Ile Asp Ser Val Thr Trp His His Thr Tyr Leu Asn Gly Arg Thr

Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile
530 535 540 543

(1) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1721
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATG CTT GTC CTC CCC TGG AAA CCG CGC CTG CAG TGG CAG CTG ATG CTG CTG 110
Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu Leu

6 10 14

Leu His Leu Val Ser Pro Phe Leu Ser Val Thr Ile Asn Ala Asn
 65 70 75 80

CTG GCG AAG GAG CGG CCG TCG CTC ATC CTC CTC GAT TCT CCA AAG TTT 80
 Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Thr Lys Leu
 65 70 75 80

CCT ACC TTG GCG AAG GCG TTG TCT CCT CGG TAC CTG AGG TTT GGT GGC 85
 Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
 85 90 95

AGC AAG ACA GAG TTC CTA ATT TTC GAT CGC AAG AAG GAA TCA ACC TTT 90
 Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe
 100 105 110

GAA GAG AAG AGT TAC TGG CAA TCT CAA CTC AAC CAG GAT ATT TGC AAA 95
 Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys
 115 120 125

TAT GGA TCC ATC CCT CCT GAT GTG GAG GAG AAG TTA CGG TTG GAA TGG 100
 Tyr Gly Ser Ile Pro Phe Asp Val Gln Glu Lys Leu Arg Leu Glu Trp
 130 135 140

CCC TAC CAG GAG CAA TTG CTA CTC CGA GAA CAC TAC CAG AAA AAG TTC 140
 Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe
 145 150 155 160

AAG AAG AGC ACC TAC TCA AGA AGC TCT GTA GAT GTG CTA TAC ACT TTT 150
 Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe
 165 170 175

GCA AAC TGC TCA GGA CTG GAC TTG ATC TTT GCG CTA AAT GCG TTA TTA 155
 Ala Asn Lys Ser Gly Leu Asp Leu Phe Gly Leu Asn Ala Leu Leu
 180 185 190

AGA ACA GGA GAT TTG CAG TGG AAC AGT TCT AAT GCT CAG TTG CTC CTG 160
 Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu
 195 200 205

ATC TAT TCT TCT TCA AAG CGG TAT AAT ACT TCT TCA GAA CTA GAT AAT 165
 Ile Tyr Thr Thr TCA AAG CGG TAT AAT ACT TCT TCA GAA CTA GAT AAT
 210 215 220

GAA ACT AAT AAT TCT TT AAT AAT ACT TAT ACT TCT ATC AAT GAT TAT 170
 Gln Pro Asn Ser Phe Leu Lys Lys Ala Asn Ile Phe Ile Asn Gly Ser
 225 230 235 240

TAT TTA GAA GAA GAT TAT ATT CAA TTT TAT AAA TTT CTA AAG AAG TCT 175
 Thr Leu Gly His Asn Trp Ile His Leu Phe Ile Leu Leu Asn Trp Ser
 245 250 255

ATC TAT TCT TCT TCA AAG CGG TAT AAT ACT TCT TCA GAA CTA GAT AAT 180
 Ile Tyr Thr Thr TCA AAG CGG TAT AAT ACT TCT TCA GAA CTA GAT AAT
 255 260 265

GTA TAC CTT CAT TGC ACA AAC ACT GAC AAT CCA AGG TAT AAA GAA GGA 1406
Val Tyr Leu His Tyr Thr Asn Thr Asp Asn Phe Arg Tyr Lys His Gly

TGT TTA GCG TAT GGT TTT TAT AAG AAG GAA GTG GAT AAA TAT GTT GTA 150
 Ala Leu Phe Tyr Phe Phe Ser Asn Lys Glu Val Asp Lys Tyr Leu Leu
 40' 4' 10' 4"

AAA AAA GAT GTC GAG GAA GAA AAT TAA ATA GAT TTA GAA GAT TTA TAA 164
Glu Lys Lys Leu Ala Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser
535 536 537

TAT AAT TTT TTT TTT ATA AAA AAT GAT AAA GTT GAT GAT TTT ATG TAA 169
Tyr Ser Phe Phe Val Ile Ala Asn Ala Lys Val Ala Ala Cys Ile
538 539 540 541

AAA TAA AAT ATA GTA GTC GTC GAA GTC 173

(2) INFORMATION FOR SEQ ID NO:12:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 824
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12

CTGGCAAGAA GGTCTGGTTS GGAGAGACGA GCTCAGTTA GGGTGGGGGT GCACCCCTTG 60
TGTCCAAACAC CTTTGCAGCT GGCTTTATGT GGCTGGATAA ATTGGGGCTG TCAGCCCAAGA 120
TGGGCAIAGA AGTCGTGATG AGGCAGTGT TCTTCGGAGC AGGCAACTAC CACTTAGTGG 180
ATGAAAACCTT TGAGCCCTTA CCTGATTAAT GGCTCTCTGT TCTGTTCAAG AAAGTGGTAG 240
GTCCACGGT GTTACTGTCA AGAGTGAAG GCCCAGACAG GAGCAAACTC CGAGTGTATC 300
TCCACTGCAC TAACGTATAT CACCAAGAT ATCAGGAAGC AGATCTAAT CTGTATGTCC 360
TGAACCTCCA TAATGTGACC AAGCAGTGA AGGTAGGCGT TCCSTTGTTC AGGAAACAG 420
TGGATACGTA CCTTCTGAAG CCTTCGGGGC CGGATGGATT ACITTCCTAAA TCTGTCCAAC 480
TGAACGCTCA AATTCTGAAG ATGGTGGATG AGCAGACCT GCCAGCTTTG ACAGAAAAAC 540
CTCTCCCGCG AGGAAGTGA CTAAGCTGCT CTGCCTTTTC CTATGGTTT TTTGTCTATA 600
GAAATGCCAA AATCGTGTCT TGTATATGAA AATAAAGGC ATACGGTACC CCTGAGACAA 660
AAGCCGAGGG GGGTGTATT CATAAAGCAA AACCTAGTT TAGGAGGCCA CCTCCTTGCC 720
GAGTTCCAGA GCTTCGGGAG GGTGGGTAC ACTTCAGTAT TACATTCAGT GTGTGTCTCT 780
CTCTAAGAAG AATACTGAG GTGGTGACAG TTAATAGTAT TGTG 824

(2) INFORMATION FOR SEQ ID NO:13:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1899
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13

AAAAA AAA AAA AAT AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA 60
AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA 120
AGGAGTAAAG GAGGAGAA AAAAGAAAAA AGGAGTAAAG GATAGGAGG AAAAGAGT 180
AGAGTCTCG ACTCTCGGT GGGGGGAGG TGGGGGGGG AGCAGGAGG TGAGCCCAAG 240
ATGCTCTCTG GGTGAAGAGT AGGAGTAAAG GAGGAGTAAAG TGTGTGTGT GTTGGGAG 300
TGTGTGTGT GTTGTGTGT GTTGTGTGT GTTGTGTGT GTTGTGTGT GTTGTGTGT 360
TGTGTGTGT GTTGTGTGT GTTGTGTGT GTTGTGTGT GTTGTGTGT GTTGTGTGT 420
ATTGAGTAAAG GAGGAGTAAAG GAGGAGTAAAG GAGGAGTAAAG GAGGAGTAAAG 480

AAAAA AAA AAA AAT AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA 60
AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA 120
AGGAGTAAAG GAGGAGAA AAAAGAAAAA AGGAGTAAAG GATAGGAGG AAAAGAGT 180

GAACTAGGCA ATGAAGCTAA CACTTTTATT AAGAACTTG ATATTTTAT CAATGGGTGG 960
 CAGTTAGGAG AAGATTATAT TAAATTATAT AAGCTT TAA GAAAGTACAC CTTCAAAAAAT 1020
 GCAAAACTCT ATGTCCTGA TTTTGGTAG CTGGAAGAA AGAGGCTAA GATGCTGAAG 1080
 AGTTTCTGA AGGCTGCTGG AGAAGTATAT GATTGAGTA CATGGCATCA CTACTATTG 1140
 AATGGAGGSA CTGCTAGCAG GGAAGATTTT CTAAGCTTG ATGATTGGA CATTTTTATT 1200
 TCACTGTGTC AAAAGATTTT TAACTGTTT GAGAAGTAA CGCTGGGAA GAACTCTG 1260
 TTAGGAGAAA CAGCTCTGT ATAGGAGG GAGAGTCT TGCTATCGA CAGCTTTGGA 1320
 CCTGGTTTA TGTGGGTGA AAAATTGPR CTGT AGGTC GAATGGGAAT AGAAGTGGTG 1380
 ATAGGGAAS TATTCTTTGG AAGAGGTAAT TATATTAG TGATGAAAA CTTGATCCT 1440
 TTACTGATT ATGGGATAT TTTCTTTC AAGAAATGG TGAGGACAA GGTGTTAATG 1500
 CCAAGCTGC AAGGTTCAAA GAGAAG AAG CTTGAGTAT ACCTTCATTG CACAAACAUT 1560
 CAAATCCAA GGTATAAGA AGGAGATTA ACTCTTATG CATAAATCT CATAAGCTG 1620
 ACAAGTACT TGGGTTTAC CTATGCTTTT TCTAA TAA G AAGTGGATAA ATACCTTCTA 1680
 AGACUTTTG GACCTCATGG ATTACTTTG AAATCTGTC AACTGAATG TCTAACTCTA 1740
 AAGATGCTGG ATGATGAAAC CTTSCCACT TTAATGAAA AACCTCTCG GCCAGGAAGT 1800
 TCACTGGCT TGGCAGCTTT CTCATAAGT TTTTCTGA TAAAGAAATGC CAAAGTTGCT 1860
 CCTTGCATCT GAAAATAAAA TATACTASTC CTGACACTG 1899

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192
 (B) TYPE: amino acid
 (C) STABILITY: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14

Met Glu Gly Ala Val Gly Gly Val Arg Arg Arg Asn Gly Ala Glu
 5 10 15
 Glu Arg Arg Lys Gly Arg Trp Gly Ser Ala Gly Gly Ser Ala Arg
 20 25 30
 Ala Leu Asp Ser Pro Leu Arg Gly Ser Trp Arg Gly Glu Gln Pro
 35 40 45
 Gly Glu Pro Lys Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro
 50 55 60
 Pro Leu Met Leu Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro
 65 70 75
 Gly Ala Leu Pro Arg Pro Ala Gln Ala Gln Asp Val Val Asp Leu
 80 85 90
 Asp Phe Phe Thr Gln Glu Pro Leu His Leu Val Ser Pro Ser Phe
 95 100 105

Leu Ser Val Thr Ile Asp Ala Asn Leu Ala Thr Arg Trp Arg Phe
 110 115 120
 Leu Ile Leu Leu Gly Ser Leu Lys Leu Arg Thr Leu Ala Arg Gly
 125 130 135
 Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly Thr Lys Thr Asp Phe
 140 145 150
 Leu Ile Phe Asp Pro Lys Lys Gln Ser Thr Phe Glu Glu Arg Ser
 155 160 165
 Tyr Thr Gln Ser Gln Val Asn Gln Asp Ile Tyr Lys Tyr Gly Ser
 170 175 180

134	137	140
Leu Ala Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu		
145	150	155
Leu Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu		
160	165	170
Leu Gly Asn Gln Pro Asn Ser Ile Leu Lys Lys Ala Asp Ile Ile		
175	180	185
Ile Asn Gly Ser Gln Leu Gly Gln Asp Tyr Ile Gln Leu His Lys		
190	195	200
Leu Leu Arg Lys Ser Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro		
205	210	215
Asp Val Gly Gln Pro Arg Ala Lys Thr Ala Lys Met Leu Lys Ser		
220	225	230
Phe Leu Lys Ala Gly Gly Gln Val Ile Asp Ser Val Thr Trp His		
235	240	245
His Tyr Tyr Leu Asn Gly Arg Thr Ala Thr Arg Gln Asp Phe Leu		
250	255	260
Asn Pro Asp Val Leu Asp Ile Phe Ile Ser Ser Val Gln Lys Val		
265	270	275
Phe Gln Val Val Glu Ser Thr Arg Pro Gly Lys Lys Val Trp Leu		
280	285	290
Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala Pro Leu Leu Ser		
295	300	305
Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys Leu Gly Leu		
310	315	320
Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val Phe Phe		
325	330	335
Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro Leu		
340	345	350
Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr		
355	360	365
Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu		
370	375	380
Arg Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys		
385	390	395
Glu Gly Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr		
400	405	410
Lys Tyr Leu Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp		
415	420	425
Leu Thr Leu Leu Arg Pro Ile His Thr His Gly Leu Leu Ser Lys		
430	435	440
Leu Val Gln Leu Asn Gln Leu Thr Leu Lys Met Val Arg Arg Gln		
445	450	455
Thr Leu Ile Ile Leu Ser Val Lys Ile Leu Arg Ile Gly Ser Ser		
460	465	470
Leu Gly Leu Pro Ala Ile Ser Tyr Ser Phe Ile Val Ile Arg Asn		
475	480	485
Ala Lys Val Ala Ala Tyr Ile		
490	495	500

Gln Glu Gln Leu Leu Leu Arg Gln His Tyr Gln Lys Lys Phe Lys	100	105	110
AAU AGU AUA UAU TUA AUA AUA UUU UUA UAU GUA UUA TAU AUA UUU	115	120	125
Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe	130	135	140
GCA AAC TGC TCA GGA CTG GAC TTG ATC TTT GGG CTA AAT GGG TTA	145	150	155
Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu	160	165	170
TTA AGA AUA GGA UAT TTG UAG TTT AAT AAT GGT CAG TTG	175	180	185
Leu Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu	190	195	200
CTC CTG GAC TAC TGT TGT TCC AAG GGG TAT AAC ATT TGT TGG GAA	205	210	215
Leu Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu	220	225	230
CTA GGC AAT GAA GGT AAC AGT TTC CTT AAG AAG GCT GAT ATT TTC	235	240	245
Leu Gly Asn Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe	250	255	260
ATC AAT GGG TCG CAG TTA GGA GAA GAT TAT ATT CAA TTG CAT AAA	265	270	275
Ile Asn Gly Ser Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys	280	285	290
CTT CTA AGA AAG TCG ACC TTC AAA AAT GCA AAA CTC TAT GGT CCT	295	300	305
Leu Leu Arg Lys Ser Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro	310	315	320
GAT GTT GGT CAG GGT CGA AGA AAG ACG GGT AAG ATG CTG AAG AGC	325	330	335
Asp Val Gly Gln Pro Arg Arg Lys Thr Ala Lys Met Leu Lys Ser	340	345	350
TTT CTG AAG GGT GGT GGA GAA GTG ATT GAT TCA GTT ACA TGG CAT	355	360	365
Phe Leu Lys Ala Gly Gly Glu Val Ile Asp Ser Val Thr Trp His	370	375	380
TAU TAU TAU UUA AUA UUA UUA AUA UUA AUA AUA AUA AUA UUU CUA	385	390	395
His Tyr Tyr Leu Asn Gly Arg Thr Ala Thr Arg Gln Arg Phe Leu	400	405	410
AAU UUA UUA UUA UUA UUA UUA UUA UUA UUA UUA UUA UUA UUA UUA	415	420	425
Asn Pro Asp Val Leu Asp Ile Phe Ile Ser Ser Val Gln Lys Val	430	435	440
TTT CAG GTT GGT GAT AAT AAT AAT AAT AAT AAT AAT AAT AAT AAT	445	450	455
Phe Gln Val Val His Ser Thr Arg Ile Gly Lys Lys Val Trp Leu	460	465	470
AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA	475	480	485
Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys	490	495	500

415	415	415
TTA GTC GGA ATG GGA ATA GAA GTG GTG ATG AAG CAA GTA TTT TTT	1575	
Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val Phe Phe		
420	420	420
GGA GCA GGA AAC TAT CAT TTA GTG GAT GAA AAT TTC GAT GCT TTA	1443	
Gly Ala Gly Asn Tyr His Leu Val Asp His Asn Phe Asp His Leu		
440	445	450
GCT GAT TAT TGG CTA TCT CTT CTG TTC AAG AAA TTG CTA GGT AAT	1485	
Phe Asp Tyr Thr Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr		
455	460	465
AAG GTG TTA ATG GGA AAG GTG CAA GGT TCA AAG AGA AAG AAG GGT	1533	
Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu		
470	475	480
GGA GTA TAC CTT CAT TGC ACA AAC AAT GAC AAT GGA AGG TAT AAA	1578	
Arg Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys		
485	490	495
GAA GGA GAT TTA ACT CTG TAT GCC ATA AAG CTC CAT AAG GTC ACC	1623	
Glu Gly Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr		
500	505	510
AAG TAC TTG CGG TTA CCC TAT CCT TTT TCT AAC AAG CAA GTG GAT	1668	
Lys Tyr Leu Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp		
515	520	525
AAA TAC CTT CTA AGA CCT TTG GGA CCT CAT GGA TTA CTT TCC AAA	1713	
Lys Tyr Leu Leu Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys		
530	535	540
TCT GTC CAA CTC AAT GGT CTA ACT CTA AAG ATG GTG GAT CAT CAA	1758	
Ser Val Gln Leu Asn Gly Leu Thr Leu Lys Met Val Asp Asp Gln		
545	550	555
AAT TTG CAA CTT TTA ATG CAA AAA CTT CTC CAA CTA GAA AAT TCA	1803	
Thr Asp Leu Ile Thr Met Gln Leu Phe Leu Arg Ile Gly Ser Ser		
560	565	570
TTA GTC TTA CAA CTT CTT TTA TAT AAT TTT TTT CTA AAT AAT AAT	1845	
Leu Gly Leu Ile Ala His Ser Tyr Ser Phe Phe Val Ile Ala Asn		
575	580	585
GAT AAA GGT GGT GGT TTT ATT TCA AAA TAA AAT ATA CTA GTC CTT	1893	
Asp Lys Val Ala Ala Lys Ile		
590	595	600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16

ATTACIATAT GGAAGCTTG GTGAGTGGC GAGCTGTA TGGCTTAAI CAGGAATTGA 60
TAAAGAATTT TGGCTCTTG ATCTTTTAA AGCTGTA TT TAGCTATAT TTA GGTAAA 120
TTTCTTACG CAAAACAAA ATATTTAAA AACTGCTT CAAAAGAA ATGAGATTTT 180
GGTGGCTA AATTGAAA CAACTTTTAT AGCTGTA T CAAAGTAA GATGAATAT 240
TGATTTGGG GTTTACTG AGGCTAGAG GATAAGG GGTATGAA ATGCTATCTG 300
GGAGTCGGAA ACGTGGGTT CCAAGAGAG GGGCAGAA CCGTGGTCA GGAAGGCTGG 360
TCCGGGATCC CCAGGCTGG TCCCGGCGG CTCTCCGG GGGCTGCTC CCAGGCTC 420
CCGGGCGCTT GGATCCGGG CATCTCGGA CCTTAAGT GGGTGTGGGT GATTCTGTAA 480
GTGAACGTA CCGTAAAG GGGCAAGTG AATAAGAA TAGGAGAG CCGGGAGGC 540
GGGGCGGT TGGATTGGA GAGCTGAG GATGAAA CAGGATTTAG AGGG 594

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17

CCGAGGAGG AGGAGATCA G 11

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18

AGGCTTCGAG CCGAGCAGCA T 11

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19

GTAATAGAG TCACTATA G 12

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20

ATTATATTT AGCTGCTT 19

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21

ATTATATTT AGCTGCTT 19

(A) LENGTH: 11
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10
 GATCTTAACT GATTTTCTT CA 11

(ii) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11
 GTAGTGATGC GATGTAAGTG AATC 14

(iii) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12
 AGGCACCCTA GAGATGTTCG AG 22

(iv) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13
 GAAGATTTCT GTTCCATGA CGTG 24

(v) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14
 TGA AAT AA TTAATACTT AACTT 25

(vi) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15

(A) LENGTH: 27
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(1) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34
 GGTAGTGGTAA AACTGTGTTG A 11

(1) INFORMATION FOR SEQ ID NO:35:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35
 AAACATTTGGT TATTAAGAC TT 11

(1) INFORMATION FOR SEQ ID NO:36:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36
 GCCAGGCTGG CGTCGATGGT GA 22

(1) INFORMATION FOR SEQ ID NO:37:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37
 GTGATGCTG ATGCACAGGA AC 22

(1) INFORMATION FOR SEQ ID NO:38:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38
 GTAATACGAC TTAATATAGG CA 22

(1) INFORMATION FOR SEQ ID NO:39:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39
 AATATATAT AACTTAT 11

(1) INFORMATION FOR SEQ ID NO:40:

(1) INFORMATION FOR SEQ ID NO:41:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41
 AATATATAT AACTTAT 11

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(1) INFORMATION FOR DEL. ID NUMBER:
(2) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 4484
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
(3) SEQUENCE DESCRIPTION: DEL. ID NUMBER

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CTTTGAGCTT	CCAAAGTGT	GGGATTAAG	GTGTGAGCA	TGAGACCCCG
CGCGCGTTT	CCATATTAGT	AACTCTGAT	TAGACACAA	GGATGCGATTA
TTTAGAAAA	TTGCAATGCT	CCATTTTCA	AATGACCGA	ACAPGTAA
GAAATTGGTA	TGACTGGGCA	TGGTACAGTG	GGCTATGCT	GGATCTGTAG
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ATCTTGACAG	ACATGTGTAA	ATCTATCTC	TACTAAAAAT	ACAAAACCAAT
TAGCGGGGG	TGATGGCAGG	CGGCTAGT	CTTAGTAAT	CGGTAGCCGTG
AGGCGAGGTA	ATGGTGTAA	CTTGAGAGG	AGAGGTGA	GTAGCCGAG
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AGAAACTTCT	GTTTTCCTAA	CTGCACTGT	CTTACATAT	TATTAAGCTG
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GCTTTTAACT	TGCTTAAGAA	TAGGTAGATC	TATGCAAAAT	ATGATAATTA
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AGGCTGGGCT	AATTTTGTGT	ATTTTTCTTA	TAGCATGTT	TGCTATGCT
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CGCTCGAAAA	TGCTGGGACT	AGAGCATTA	TGCGATCA	GGATGCGAT
AGGATGCGTG	GGCTGATTA	TGAAATTA	ATATGCTAT	CAAAATAATG
TATTTTATTT	TGTTTGCTTA	TTTGTGAC	AATGTAAAT	GGAAATATCT
AAGGTGTTTG	TGTTTATTTG	CTTACTCAAC	CAATATTTAT	TAGACTCTTA
CTAAGGACGA	ACATATGATC	ATCTGAGAG	TATGCTATT	ATAGCTGTGT
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CGAATGTGTA	GCAATATTA	AATATATTA	ATATATTAAT	CTTAGCAGAG
TTTAAAGAT	ATTATTAAT	TATGAGAT	CTTAAAGAA	CTTAAATG

CGA GAA T	TA ATT TA	T AAA A A	T TAT T	TA ATT
CTAAA T	TA ATT TA	AT T A A	TT AAT	TAAT TA
CTTAA TA	ATA T T	A A T T	T TAT T	TAAT TA
TA A TAT	ATT T A	TT T A A	CTAAA TA	TAAT TA
TA TAT	TATTA T	TA A A	A T T	TAAT TA
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AACGAAG	ATAATG C	AAGAG AA	TTTGAAG	CTGAAG A
CATCTAGT	CTATCTA	CA TTTGT	CTCTCTA	CTCTGAGT
T AAGATT	GAG AA TA	A T TTA	ATTATTAAT	ATTCTTAAT
TAAGAT	ATAAAGATT	TT T T T	TAT T T	ATTCTTAAT
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| CAATCGGCG | GTAAGATAT | GGTA TGG | AA TTATCT | AGTGGCT | 26900 |
| TAGAAATCT | GGAT TGA | TGCA AAT | AG TGGCT | ATA TGA | 26950 |
| ATCAATCA | CTGGTACCT | TAGAAAT | TTTATGTA | AT TCTT | 27000 |
| CTCTTTTG | CGAGCTGG | CTT TAT | TG TGGT | TAG ATCT | 27050 |
| TCATCTTGG | CTCTT AGAG | TG TCTT | AT TGAAG | ATG TGA | 27100 |
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| TCTTTATG | TG AATCT | ATTAAGT | CT TCT | TATATAGAT | 27200 |
| TTTAAAAA | AA TAAAT | TG TCT | TATATAT | AT TAT TGA | 27250 |
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| TTT TAT | CTATAT | AA TAT | TT TAT | ATATAT | 27350 |
| ATG GAT | TTTAT ATAT | ATTT TTTT | AT TAT | ATATAT | 27400 |
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| ATGAGGCTGT | TATCATTTTT | CTTTACGAT | CAGAGCTGA | ATGCAATTT | 3080 |
| TTTCAAA | TACCTAAT | TAGTCAAG | AATGAAGAA | CAAGCTTAA | 3085 |
| CTTTAAG | CAAGATGAT | TACAGAT | CTATCTTT | TATTTAT | 3090 |
| ATTTTAT | GTATATTT | TTTAAAT | TTTTTAT | CACTTCTT | 3095 |
| CTTTTAA | CAAGAGAAA | TTTATAG | CTTTAAAT | CACTTTAG | 3100 |
| CAAGATTA | TATGATAT | TAATAG | CTTTTAA | CAAGAGAT | 3105 |
| CTTTTAA | ATTAATTAAT | CAAGAGAA | ATATATAAT | CAAGAGAT | 3110 |
| ATATATTT | CAATTTAA | TTTATAT | TTTATTA | CAAGAA | 3115 |
| ATTTTAT | TCTCTCT | ATTTT | CAATTAAT | TTTATAT | 3120 |
| CAAGATTA | ATTAATTT | TTTATAT | TTTTT | CAAGAA | 3125 |
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(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2396
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:43:

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 2. The sequence of the DNA molecule is as follows: AATCTCTCA ATCTCTCAAA CAGCTATCT CAGCTATCT CAGCTATCT 1000

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GTCTCTT 629 GTTCTT 630 GTTCTT 631 GTTCTT 632 GTTCTT 633 GTTCTT 634
GTCTCTT 635 GTTCTT 636 GTTCTT 637 GTTCTT 638 GTTCTT 639 GTTCTT 640
GTCTCTT 641 GTTCTT 642 GTTCTT 643 GTTCTT 644 GTTCTT 645 GTTCTT 646
GTCTCTT 647 GTTCTT 648 GTTCTT 649 GTTCTT 650 GTTCTT 651 GTTCTT 652
GTCTCTT 653 GTTCTT 654 GTTCTT 655 GTTCTT 656 GTTCTT 657 GTTCTT 658
GTCTCTT 659 GTTCTT 660 GTTCTT 661 GTTCTT 662 GTTCTT 663 GTTCTT 664
GTCTCTT 665 GTTCTT 666 GTTCTT 667 GTTCTT 668 GTTCTT 669 GTTCTT 670
GTCTCTT 671 GTTCTT 672 GTTCTT 673 GTTCTT 674 GTTCTT 675 GTTCTT 676
GTCTCTT 677 GTTCTT 678 GTTCTT 679 GTTCTT 680 GTTCTT 681 GTTCTT 682
GTCTCTT 683 GTTCTT 684 GTTCTT 685 GTTCTT 686 GTTCTT 687 GTTCTT 688
GTCTCTT 689 GTTCTT 690 GTTCTT 691 GTTCTT 692 GTTCTT 693 GTTCTT 694
GTCTCTT 695 GTTCTT 696 GTTCTT 697 GTTCTT 698 GTTCTT 699 GTTCTT 700
GTCTCTT 701 GTTCTT 702 GTTCTT 703 GTTCTT 704 GTTCTT 705 GTTCTT 706
GTCTCTT 707 GTTCTT 708 GTTCTT 709 GTTCTT 710 GTTCTT 711 GTTCTT 712
GTCTCTT 713 GTTCTT 714 GTTCTT 715 GTTCTT 716 GTTCTT 717 GTTCTT 718
GTCTCTT 719 GTTCTT 720 GTTCTT 721 GTTCTT 722 GTTCTT 723 GTTCTT 724
GTCTCTT 725 GTTCTT 726 GTTCTT 727 GTTCTT 728 GTTCTT 729 GTTCTT 730
GTCTCTT 731 GTTCTT 732 GTTCTT 733 GTTCTT 734 GTTCTT 735 GTTCTT 736
GTCTCTT 737 GTTCTT 738 GTTCTT 739 GTTCTT 740 GTTCTT 741 GTTCTT 742
GTCTCTT 743 GTTCTT 744 GTTCTT 745 GTTCTT 746 GTTCTT 747 GTTCTT 748
GTCTCTT 749 GTTCTT 750 GTTCTT 751 GTTCTT 752 GTTCTT 753 GTTCTT 754
GTCTCTT 755 GTTCTT 756 GTTCTT 757 GTTCTT 758 GTTCTT 759 GTTCTT 760
GTCTCTT 761 GTTCTT 762 GTTCTT 763 GTTCTT 764 GTTCTT 765 GTTCTT 766
GTCTCTT 767 GTTCTT 768 GTTCTT 769 GTTCTT 770 GTTCTT 771 GTTCTT 772
GTCTCTT 773 GTTCTT 774 GTTCTT 775 GTTCTT 776 GTTCTT 777 GTTCTT 778
GTCTCTT 779 GTTCTT 780 GTTCTT 781 GTTCTT 782 GTTCTT 783 GTTCTT 784
GTCTCTT 785 GTTCTT 786 GTTCTT 787 GTTCTT 788 GTTCTT 789 GTTCTT 790
GTCTCTT 791 GTTCTT 792 GTTCTT 793 GTTCTT 794 GTTCTT 795 GTTCTT 796
GTCTCTT 797 GTTCTT 798 GTTCTT 799 GTTCTT 800 GTTCTT 801 GTTCTT 802
GTCTCTT 803 GTTCTT 804 GTTCTT 805 GTTCTT 806 GTTCTT 807 GTTCTT 808
GTCTCTT 809 GTTCTT 810 GTTCTT 811 GTTCTT 812 GTTCTT 813 GTTCTT 814
GTCTCTT 815 GTTCTT 816 GTTCTT 817 GTTCTT 818 GTTCTT 819 GTTCTT 820
GTCTCTT 821 GTTCTT 822 GTTCTT 823 GTTCTT 824 GTTCTT 825 GTTCTT 826
GTCTCTT 827 GTTCTT 828 GTTCTT 829 GTTCTT 830 GTTCTT 831 GTTCTT 832
GTCTCTT 833 GTTCTT 834 GTTCTT 835 GTTCTT 836 GTTCTT 837 GTTCTT 838
GTCTCTT 839 GTTCTT 840 GTTCTT 841 GTTCTT 842 GTTCTT 843 GTTCTT 844
GTCTCTT 845 GTTCTT 846 GTTCTT 847 GTTCTT 848 GTTCTT 849 GTTCTT 850
GTCTCTT 851 GTTCTT 852 GTTCTT 853 GTTCTT 854 GTTCTT 855 GTTCTT 856
GTCTCTT 857 GTTCTT 858 GTTCTT 859 GTTCTT 860 GTTCTT 861 GTTCTT 862
GTCTCTT 863 GTTCTT 864 GTTCTT 865 GTTCTT 866 GTTCTT 867 GTTCTT 868
GTCTCTT 869 GTTCTT 870 GTTCTT 871 GTTCTT 872 GTTCTT 873 GTTCTT 874
GTCTCTT 875 GTTCTT 876 GTTCTT 877 GTTCTT 878 GTTCTT 879 GTTCTT 880
GTCTCTT 881 GTTCTT 882 GTTCTT 883 GTTCTT 884 GTTCTT 885 GTTCTT 886
GTCTCTT 887 GTTCTT 888 GTTCTT 889 GTTCTT 890 GTTCTT 891 GTTCTT 892
GTCTCTT 893 GTTCTT 894 GTTCTT 895 GTTCTT 896 GTTCTT 897 GTTCTT 898
GTCTCTT 899 GTTCTT 900 GTTCTT 901 GTTCTT 902 GTTCTT 903 GTTCTT 904
GTCTCTT 905 GTTCTT 906 GTTCTT 907 GTTCTT 908 GTTCTT 909 GTTCTT 910
GTCTCTT 911 GTTCTT 912 GTTCTT 913 GTTCTT 914 GTTCTT 915 GTTCTT 916
GTCTCTT 917 GTTCTT 918 GTTCTT 919 GTTCTT 920 GTTCTT 921 GTTCTT 922
GTCTCTT 923 GTTCTT 924 GTTCTT 925 GTTCTT 926 GTTCTT 927 GTTCTT 928
GTCTCTT 929 GTTCTT 930 GTTCTT 931 GTTCTT 932 GTTCTT 933 GTTCTT 934
GTCTCTT 935 GTTCTT 936 GTTCTT 937 GTTCTT 938 GTTCTT 939 GTTCTT 940
GTCTCTT 941 GTTCTT 942 GTTCTT 943 GTTCTT 944 GTTCTT 945 GTTCTT 946
GTCTCTT 947 GTTCTT 948 GTTCTT 949 GTTCTT 950 GTTCTT 951 GTTCTT 952
GTCTCTT 953 GTTCTT 954 GTTCTT 955 GTTCTT 956 GTTCTT 957 GTTCTT 958
GTCTCTT 959 GTTCTT 960 GTTCTT 961 GTTCTT 962 GTTCTT 963 GTTCTT 964
GTCTCTT 965 GTTCTT 966 GTTCTT 967 GTTCTT 968 GTTCTT 969 GTTCTT 970
GTCTCTT 971 GTTCTT 972 GTTCTT 973 GTTCTT 974 GTTCTT 975 GTTCTT 976
GTCTCTT 977 GTTCTT 978 GTTCTT 979 GTTCTT 980 GTTCTT 981 GTTCTT 982
GTCTCTT 983 GTTCTT 984 GTTCTT 985 GTTCTT 986 GTTCTT 987 GTTCTT 988
GTCTCTT 989 GTTCTT 990 GTTCTT 991 GTTCTT 992 GTTCTT 993 GTTCTT 994
GTCTCTT 995 GTTCTT 996 GTTCTT 997 GTTCTT 998 GTTCTT 999 GTTCTT 1000

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(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 535
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) SEQUENCE DESCRIPTION: SEQ ID NO:44

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Met Leu Arg Leu Leu Leu Leu Trp Leu Trp Gly Pro Leu Gly Ala
      1              10              15
Leu Ala Gly Gly Ala Pro Ala Gly Thr Ala Pro Thr Arg Arg Val
      21              30              35
Val Arg Leu Gly Ile Trp Thr Leu Arg Pro Leu Arg Leu Val Ser
      41              50              55
Pro Arg Pro Leu Leu Thr Thr Leu Arg Ala Pro Leu Arg Arg
      61              70              75
Pro Arg Phe Leu Thr Phe Leu Gly Ser Pro Arg Leu Arg Ala Leu
      81              90              95
Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly Thr Lys
     101             110             115
Thr Arg Phe Leu Ile Phe Arg Pro Arg Leu Gly Leu Thr Ser Gly

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| | | | |
|-------------------------------------------------------------|-----|-----|-----|
| Glu Phe Lys Asn Ser Thr Tyr Ser Ala Ser Ser Val Asp Met Leu | 118 | 119 | 120 |
| Tyr Ser Phe Ala Lys Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu | 121 | 122 | 123 |
| Asn Ala Leu Leu Ala Thr Phe Asp Leu Arg Ile Asn Ser Ser Asp | 124 | 125 | 126 |
| Ala Gln Leu Leu Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile | 127 | 128 | 129 |
| Ser Trp Glu Leu Gly Asn Gln Pro Arg Ser Phe Trp Lys Lys Ala | 130 | 131 | 132 |
| His Ile Leu Ile Asp Gly Leu Gln Leu Gly Gln Asp Phe Val Glu | 133 | 134 | 135 |
| Leu His Lys Leu Leu Gln Arg Ser Ala Phe Gln Asn Ala Lys Leu | 136 | 137 | 138 |
| Tyr Gly Pro Asp Ile Gly Gln Pro Arg Gly Lys Thr Val Lys Leu | 139 | 140 | 141 |
| Leu Arg Ser Phe Leu Lys Ala Gly Gly Glu Val Ile Asp Ser Leu | 142 | 143 | 144 |
| Thr Trp His His Tyr Tyr Leu Asn Gly Arg Ile Ala Thr Lys Glu | 145 | 146 | 147 |
| Asp Phe Leu Ser Ser Asp Ala Leu Asp Thr Phe Ile Leu Ser Val | 148 | 149 | 150 |
| Gln Lys Ile Leu Lys Val Thr Lys Glu Ile Thr Pro Gly Lys Lys | 151 | 152 | 153 |
| Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala Pro | 154 | 155 | 156 |
| Leu Leu Ser Asn Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys | 157 | 158 | 159 |
| Leu Gly Leu Ser Ala Gln Met Gly Ile Glu Val Val Met Arg Gln | 160 | 161 | 162 |
| Val Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe | 163 | 164 | 165 |
| Glu Pro Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu | 166 | 167 | 168 |
| Val Gly Pro Arg Val Leu Leu Ser Arg Val Lys Gly Pro Asp Arg | 169 | 170 | 171 |
| Ser Lys Leu Arg Val Tyr Leu His Cys Thr Asn Val Tyr His Pro | 172 | 173 | 174 |
| Arg Tyr Gln Glu Gly Asp Leu Thr Leu Tyr Val Leu Asn Leu His | 175 | 176 | 177 |
| Asn Val Thr Lys His Leu Lys Val His Phe Thr Phe Phe Arg Lys | 178 | 179 | 180 |
| His Val Arg Ser Tyr Leu Leu Gly His Ser Gly His Arg Gly Leu | 181 | 182 | 183 |
| Leu Ser Lys Ser Val Gln Leu Asn Gly Gln Ile Leu Lys Met Val | 184 | 185 | 186 |
| Asp Gln Gln Thr Leu His Ala Leu Thr Gln Lys Phe Leu Pro Ala | 187 | 188 | 189 |
| Gly Tyr Ala Leu Ser Leu His Ala His Ser Tyr Gly His His Val | 190 | 191 | 192 |

1. The amino acid sequence of the protein is:

 Asn Val Thr Lys His Leu Lys Val His Phe Thr Phe Phe Arg Lys

 His Val Arg Ser Tyr Leu Leu Gly His Ser Gly His Arg Gly Leu

 Leu Ser Lys Ser Val Gln Leu Asn Gly Gln Ile Leu Lys Met Val

 Asp Gln Gln Thr Leu His Ala Leu Thr Gln Lys Phe Leu Pro Ala

 Gly Tyr Ala Leu Ser Leu His Ala His Ser Tyr Gly His His Val

GGT AGA GGC TTA TCT ACT GAA TAC TTG ACA TTT GGC GGC ACA AAG 40
Ala Arg Gly Leu Ser Ile Ala Thr Leu Arg Ile Gly Gly Thr Asp

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GAA | AGA | AAT | TAC | TGG | AAA | TCT | GAA | GTC | AAU | UAT | GAT | ATT | TGT | AGG | 953 |
| Glu | Arg | Asn | Tyr | Trp | Lys | Ser | Gln | Val | Asn | His | Asp | Ile | Cys | Arg | |
| | | | | 11 | | | | 111 | | | | | 112 | | |

GAG TTT AAG AAT AGG AAT TAC TTA AGA AGT TTA GTT GAG ATG CTG 1377
Gln Ile Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Met Leu
177 182 187

TAC AGT TTT GGG AAG TGG TGG GGG TTA GAG GTG ATG TTT GGT CTA 1132
Tyr Ser Ile Ala Lys Lys Ser Gly Leu Asp Leu Ile Ile Gly Leu
178 179 180 181 182 183 184 185 186 187 188 189

AAT GGG TTA CTA GGA ACC GGA GAG TTA GGG TGG AAG AGG TCG AAG 1178
Asn Ala Leu Leu Arg Thr Pro Asp Leu Arg Trp Asn Ser Ser Asn
188 189 190 191 192 193 194 195 196 197 198 199

GCG CAG CTT CTC CTT GAG TAC TCG TTT TCG AAG GGT TAT AAT ATC 1373
Ala Gln Leu Leu Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile
200 205 210

TCC TGG GAA CTG GGC AAT GAG CCC AAC AGT TTC TGG AAG AAA GCT 1268
Ser Trp Glu Leu Gly Asn Glu Pro Asn Ser Phe Trp Lys Lys Ala
215 220 225

GAC ATT CTC ATC GAT GGG TTG CAG TTA GGA CAA GAC TTT GTG GAG 1313
His Ile Leu Ile Asp Gly Leu Gln Leu Gly Glu Asp Phe Val Glu
230 235 240

TTG CAT AAA CTT CTA CAA AGG TCA GCT TTC CAA AAT GCA AAA CTC 1358
Leu His Lys Leu Leu Gln Arg Ser Ala Phe Gln Asn Ala Lys Leu
245 250 255

TAT GGT GGT GAC ATC GGT CAG GGT CGA GGG AAG ACA GTT AAA CTG 1403
Tyr Gly Pro Asp Ile Gly Gln Pro Arg Gly Lys Thr Val Lys Leu
260 265 270

CTG AGG AGT TTC CTG AAG GCT GGC GGA GAA GTG ATC GAC TCT CTT 1448
Leu Arg Ser Phe Leu Lys Ala Gly Gly Glu Val Ile Asp Ser Leu
275 280 285

ACA TGG CAT CAC TAT TAC TTG AAT GGA GGC ATC GGT ACC AAA GAA 1493
Thr Trp His His Tyr Tyr Leu Asn Gly Arg Ile Ala Thr Lys Glu
290 295 300

ATG TTT TTA AAT TTT AAT GAT TTA GAT AAT TTT ATT TTT TTT GTT 1538
Met Ile Leu Ser Ser Arg Ala Leu Arg Thr Ile Ile Leu Ser Val
305 310 315

CAA AAA ATT CTG AAG GTC ACT AAA GAG ATC ACA GGT GGC AAG AAG 1583
Gln Lys Ile Leu Lys Val Thr Lys Glu Ile Thr Pro Gly Lys Lys
320 325 330

CTT TAT TTT GGA GAT AAT AAT TTA ATT TAT GGT TTT GGT TTA TTT 1628
Leu Tyr TTT GGA GAT AAT AAT TTA ATT TAT GGT TTT GGT TTA TTT
335 340 345 350 355 360 365 370 375 380 385 390

TTG GGG CTG TCA GGC CAG ATG GGT ATA GAA GTC GTG ATG AGG CAG 1718
 Leu Gly Leu Ser Ala Gln Met Gly Ile Gln Val Val Met Arg Gln
 375 376 377

GTC TTC TTC GGA GGA GGT AAC TAC GAT PTA GTG GAT GAA AAT TTT 1723
 Val Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Gln Asn Ile
 378 379 380

GAG COT TTA CCT GAT TAC TGG CTC TCT CTT CTG TTC AAG AAA CTG 1808
 Glu Pro Leu Pro Asp Tyr Trp Leu Ser Leu Leu Ile Lys Lys Leu
 395 400 405

GTA GGT GGT AGG GTG TTA CTC TCA AGA GTG AAA GGT GGA GGC AGG 1853
 Val Gly Pro Arg Val Leu Leu Ser Arg Val Lys Gly Pro Asp Arg
 410 415 420

AGC AAA CTC CGA GTG TAT CTC CAC TGC ACT AAC GTC TAT CAC CGA 1898
 Ser Lys Leu Arg Val Tyr Leu His Cys Thr Asn Val Tyr His Pro
 425 430 435

CGA TAT CAG GAA GGA GAT CTA ACT CTG TAT GTC CTG AAC CTC CAT 1943
 Arg Tyr Gln Glu Gly Asp Leu Thr Leu Tyr Val Leu Asn Leu His
 440 445 450

AAT GTC ACC AAG CAC TTG AAG GTA CCG COT CCG TTG TTC AGG AAA 1988
 Asn Val Thr Lys His Leu Lys Val Pro Pro Pro Leu Phe Arg Lys
 455 460 465

CGA GTG GAT ACG TAC CTT CTG AAG COT TCG GGG CCG GAT GGA TTA 2033
 Pro Val Asp Thr Tyr Leu Leu Lys Pro Ser Gly Pro Asp Gly Leu
 470 475 480

CTT TCC AAA TCT GTC CAA CTG AAC GGT GAA ATT CTG AAG ATG GTG 2078
 Leu Ser Lys Ser Val Gln Leu Asn Gly Gln Ile Leu Lys Met Val
 485 490 495

GAT GAG CAG ACC CTG CCA GCT TTG ACA GAA AAA COT CTC CCG GCA 2123
 Asp Glu Gln Thr Leu Pro Ala Leu Thr Glu Lys Pro Leu Pro Ala
 500 505 510

GGA AGT GGA CTA AAT CTG CTT GCT TTT TAT GAT TTT TTT GTT 2168
 Gly Arg Ala Leu Ser Leu Ile Ala Ile Ser Tyr Gly Ile Ile Val
 515 520 525

ATA AGA AAT GCC AAA ATC GGT GCT TGT ATA TGA AAA TAA AAG GGA 2213
 Ile Arg Asn Ala Lys Ile Ala Ala Cys Ile
 530 535

TAT GGT AAT CTT GAT ATA AAA TTT GAT GAT GTT GTT ATT GAT AAA 2258
 Tyr Gly Asn Leu Asp Ile AAA TTT GAT GAT GTT GTT ATT GAT AAA
 540 545

(k) TYPE: nucleic acid
 (l) STRANDEDNESS: double
 (m) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46

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CTTGGTATG TGTATGATG CTTCTGCTG CTTCTGCTG CTTCTGCTG    50
ATTGACTGAG GGTGGGAGGG CTTCTGCTGAA AGAGGTGCTG GATTGGAGT    100
TTTAGAGTAA GAGGCTATTG CAAAGGTGA CTTCTGCTGTT CTTCTGCTG    150
ATTATGAGAG CCAAGTGTGG CAAGAGCTT CTTCTGCTG CTTCTGCTG    200
CTCTCCAGGG CTTCTGAGGG TTTCTAGAGG CTTATCTGCT GCTGATTTGA    250
GATTTCGGGG CAAAGAAGAT GATTCTTA TTTTGTATG CAAAGAAGAA    300
CTTACTGTG AAGAAAGAG TTAATGAA TTTAAGAGA AATATATAT    350
TTGCGGTCT GATCGGTCT CAGCTGAGT GTGA                385
  
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(j) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(a) LENGTH: 541
 (b) TYPE: nucleic acid
 (c) STRANDEDNESS: double
 (d) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47

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AAATCAGGAC ATATCTTGA CTTATTGCG TCTTGTGCTAT ATTGGAGGCA    50
TTTGTATTGA TTTTGAATAA CTTCTGAAAT AGTGCATGCA AAGTGCTAAG    100
CGTCATTTGC CACATGCTGC CATTAAGTGT CACCACCTGC AGTGGTCTAG    150
TTAGAGAACA CCGCAATGGA TGITAACACT GAAGCGCGTG CCCCGCCCTC    200
CCGAGGCTCT GGATCCAGCG TTGAAGCTTG CCCCGCCCTC CCGAGGCTCT    250
GGATCCAGCA CTGGAGCATG CCCCGCCCTC CCGAGGCTCT GGAGCTTGCT    300
AAGGAGTGGG CTGCTACGCG CTGGGCTTTT GCTTTATTCT TATCAATGAC    350
AGCCCTGACC GCTTTGCTCT CAGGGGTAAT GTAATGCTT TTATTTTCAI    400
ATACAAGCTG CGATTTTGGC ATTTCTTATG AAAAAAACC CATAGGAAAA    450
GGCGGGCAGG CTTAGTGAGG TTCTGCGGG GAGAGTTTTT TCTGTTAGAG    500
CTGGCANGGT CTGCTCATCG ACCATCTTCA GGCTCGTGC C                541
  
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